comparing the first sequenced region with historical sequence data stored in a database;

determining a measure of phylogenetic relatedness between the [microorganism sample] first sequenced region of the microorganism sample and [a plurality of historical samples stored in the database] the historical sequence data stored in the database based upon differences between the first sequenced region of the microorganism and the historical sequence data; [and]

providing infection control information based on the phylogenetic relatedness determination; and [to the remote facility, thereby allowing the remote facility to use]

utilizing the infection control information in the real-time [to] control or [prevent] prevention of the spread of an infection.

3. (Amended) The method of claim [2] 1, wherein the database is a centralized database located in an infection control facility, the infection control facility transmitting infection control information to the remote facility via a computer network.

4. (Amended) The method of claim 1, wherein the database is located in the same location as [the remote facility] where the microorganism sample is obtained.

5. (Amended) The method of claim 1, wherein the first region that is sequenced is a region [that has been identified to have] having a mutation rate which is suitably fast for performing real-time infection control.

6. (Amended) The method of claim [4] 1, wherein the first region that is sequenced is a repeat region.

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8. (Amended) The method of claim 7, wherein [a sample of a] the microorganism sample is obtained from a prospective patient before the patient is admitted to [the health care facility] and exposed to patients in a health care facility.

11. (Amended) The method of claim 10, further including:

transmitting the patient's medical history to the [centralized] database without transmitting sensitive patient information; and

storing the sensitive patient information in a local database [at the health care facility] remote from the database to which the patient's medical history is transmitted.

12. (Amended) The method of claim 1, wherein the step of sequencing comprises either:

a) sequencing the microorganism sample at [the] a remote facility and transmitting the resulting sequence data to the [centralized] database via a computer network; or

b) sending the microorganism sample to an infection control facility associated with the [centralized] database, sequencing the microorganism at the infection control facility, and storing the sequence data in the [centralized] database.

16. (Amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the microorganism sample and a historical sample stored in the database includes:

identifying repeat sequences in the sequenced first region of the microorganism sample and the historical samples; and

comparing [the] a similarity between a repeat motif in the microorganism sample

sequence and a repeat motif in a corresponding historical sample sequence; and

determining a repeat motif cost that is a measure of phylogenetic [distance] relatedness

between the samples based on the similarity between the repeat motifs.

17. (Amended) The method of claim 16, further including:

comparing [the] a similarity between individual base-pair sequence in the microorganism

sample and the individual base-pair sequence in the corresponding historical sample; and

determining a point mutation cost that is measure of phylogenetic [distance] relatedness

between the samples based on the similarity between the individual base pair sequences.

19. (Amended) The method of claim 16, further including:

calculating a phylogenetic [distance] relatedness between the sample and a historical

sample, wherein the deletion or insertion of a repeat sequence is treated as a single event.

21. (Amended) The method of claim 1, wherein the step of determining the

phylogenetic relatedness between the first sequenced region of the microorganism sample and

the historical [samples] sequence data stored in the database includes at least one of:

comparing the first sequenced region of the microorganism sample to historical sequence

data representing samples obtained from the same [remote facility] location as the

microorganism sample, thereby [to] determining a local phylogenetic relatedness;

comparing the first sequenced region of the microorganism sample to historical sequence

data representing samples obtained from the same geographical region as where the

microorganism sample was taken, thereby determining [to determine] a regional phylogenetic

relatedness; and

comparing the first sequenced region of the microorganism sample to historical sequence

data representing global historical samples, thereby determining [to determine] a global

phylogenetic relatedness.

22. (Amended) The method of claim 1, further including:

transmitting the physical location of a patient from which the microorganism sample is

taken;

storing the physical location in the [centralized] database; and

determining a path of transmission of an infection based on the phylogenetic relatedness

determination and the physical location of the patient.

23. (Amended) The method of claim 22, further including:

storing a map of the [health care facility] physical location in the [centralized] database;

and

determining the spread of the infection based on the map of the [health care facility]

physical location.

24. (Amended) The method of claim 23, further including:

sensing the patient's physical location[; and] prior to transmitting the patient's physical

location.

[transmitting the patient's physical location to the centralized server.]

25. (Amended) The method of claim 1, further including:

determining the virulence of the microorganism by retrieving the virulence data of identical or similar microorganisms from the [centralized] database; and

transmitting virulence information to [the remote facility] a location where the microorganism sample was obtained.

26. (Amended) The method of claim 1, [further including] wherein the step of providing infection control information comprises:

determining drug resistance and treatment information of the microorganism by retrieving drug information data of identical or similar microorganisms from the [centralized] database; and

transmitting the drug information data to [the health care facility] a location where the microorganism sample was obtained.

27. (Amended) The method of claim 1, further including:

determining whether [the health care facility] a location where the microorganism sample was obtained has [a potential] an outbreak problem; and

transmitting an outbreak warning to the [health care facility] location where the microorganism sample was obtained.

28. (Amended) The method of claim 1, further including:

sequencing a second region of the nucleic acid of the microorganism sample; and

comparing the second sequenced region with corresponding historical sequence data stored in [a centralized] the database;

determining a measure of phylogenetic relatedness between the microorganism sample and [historical samples] the corresponding historical sequence data stored in the [centralized] database based on the comparison of the second sequenced region.

30. (Amended) The method of claim 28, further including:

identifying a first level of subspecies of the microorganism sample based on the first sequenced region; and

identifying a second level of subspecies of the microorganism sample based on the second sequenced region.

32. (Amended) A system for performing real-time infection control over a computer network, comprising:

a computer network;

a centralized database;

a remote facility connected to the computer network, the remote facility obtaining a sample of a microorganism;

a server connected to the computer network, the server

receiving sequence data for a first sequenced region of a nucleic acid from the microorganism sample,

accessing the centralized database and comparing the first sequenced region with historical sequence data stored in the centralized database,

determining a measure of phylogenetic relatedness between the microorganism sample and historical samples stored in the centralized database, and

transmitting infection control information based on the phylogenetic relatedness determination to the remote facility over the computer network, thereby allowing the [health care] remote facility to use the infection control information to control or prevent the spread of an infection.

33. (Amended) Computer executable software code stored on a computer readable medium, performing a method of real-time infection control over a computer network, comprising:

obtaining a sample of a microorganism [at a remote facility];

sequencing a first region of a nucleic acid from the microorganism sample;

comparing the first sequenced region with historical sequence data stored in a centralized database;

determining a measure of phylogenetic relatedness between the microorganism sample and historical samples stored in the centralized database; and

providing infection control information based on the phylogenetic relatedness determination [to the remote facility], thereby allowing [the remote facility to] use of the infection control information to control or prevent the spread of an infection.

Clean copy of amended claims:

1. (Amended) A method of performing real-time infection control, comprising:

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obtaining a sample of a microorganism;

sequencing a first region of a nucleic acid from the microorganism sample;

comparing the first sequenced region with historical sequence data stored in a database;

determining a measure of phylogenetic relatedness between the first sequenced region of the microorganism sample and the historical sequence data stored in the database based upon differences between the first sequenced region of the microorganism and the historical sequence data;

providing infection control information based on the phylogenetic relatedness determination; and utilizing the infection control information in the real-time control or prevention of the spread of an infection.

3. (Amended) The method of claim 1, wherein the database is a centralized database located in an infection control facility, the infection control facility transmitting infection control information to the remote facility via a computer network.

4. (Amended) The method of claim 1, wherein the database is located in the same location as where the microorganism sample is obtained.

5. (Amended) The method of claim 1, wherein the first region that is sequenced is a region having a mutation rate which is suitably fast for performing real-time infection control.

6. (Amended) The method of claim 1, wherein the first region that is sequenced is a repeat region.

8. (Amended) The method of claim 7, wherein the microorganism sample is obtained from a prospective patient before the patient is admitted to and exposed to patients in a health care facility.

11. (Amended) The method of claim 10, further including:

transmitting the patient's medical history to the database without transmitting sensitive patient information; and

storing the sensitive patient information in a local database at the remote from the database that the patient's medical history is transmitted to.

12. (Amended) The method of claim 1, wherein the step of sequencing comprises either:

a) sequencing the microorganism sample at a remote facility and transmitting the resulting sequence data to the database via a computer network; or

b) sending the microorganism sample to an infection control facility associated with the database, sequencing the microorganism at the infection control facility, and storing the sequence data in the database.

16. (Amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the microorganism sample and a historical sample stored in the database includes:

identifying repeat sequences in the sequenced first region of the microorganism sample and the historical samples; and

comparing a similarity between a repeat motif in the microorganism sample sequence and a repeat motif in a corresponding historical sample sequence; and

determining a repeat motif cost that is a measure of phylogenetic relatedness between the samples based on the similarity between the repeat motifs.

17. (Amended) The method of claim 16, further including:

comparing a similarity between individual base-pair sequence in the microorganism sample and the individual base-pair sequence in the corresponding historical sample; and

determining a point mutation cost that is measure of phylogenetic relatedness between the samples based on the similarity between the individual base pair sequences.

19. (Amended) The method of claim 16, further including:

calculating a phylogenetic relatedness between the sample and a historical sample, wherein the deletion or insertion of a repeat sequence is treated as a single event.

21. (Amended) The method of claim 1, wherein the step of determining the phylogenetic relatedness between the first sequenced region of the microorganism sample and the historical sequence data stored in the database includes at least one of:

comparing the first sequenced region of the microorganism sample to historical sequence data representing samples obtained from the same location as the microorganism sample, thereby determining a local phylogenetic relatedness;

comparing the first sequenced region of the microorganism sample to historical sequence data representing samples obtained from the same geographical region as where the

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microorganism sample was taken, thereby determining a regional phylogenetic relatedness; and

comparing the first sequenced region of the microorganism sample to historical sequence data representing global historical samples, thereby determining a global phylogenetic relatedness.

22. (Amended) The method of claim 1, further including:

transmitting the physical location of a patient from which the microorganism sample is taken;

storing the physical location in the database; and

determining a path of transmission of an infection based on the phylogenetic relatedness determination and the physical location of the patient.

23. (Amended) The method of claim 22, further including:

storing a map of the physical location in the database; and

determining the spread of the infection based on the map of the physical location.

24. (Amended) The method of claim 23, further including:

sensing the patient's physical location prior to transmitting the patient's physical location.

25. (Amended) The method of claim 1, further including:

determining the virulence of the microorganism by retrieving the virulence data of identical or similar microorganisms from the database; and

transmitting virulence information to a location where the microorganism sample was

obtained.

26. (Amended) The method of claim 1, wherein the step of providing infection control information comprises:

determining drug resistance and treatment information of the microorganism by retrieving drug information data of identical or similar microorganisms from the database; and

transmitting the drug information data to a location where the microorganism sample was obtained.

27. (Amended) The method of claim 1, further including:

determining whether a location where the microorganism sample was obtained has an outbreak problem; and

transmitting an outbreak warning to the location where the microorganism sample was obtained.

28. (Amended) The method of claim 1, further including:

sequencing a second region of the nucleic acid of the microorganism sample; and

comparing the second sequenced region with corresponding historical sequence data stored in the database;

determining a measure of phylogenetic relatedness between the microorganism sample and the corresponding historical sequence data stored in the database based on the comparison of the second sequenced region.

30. (Amended) The method of claim 28, further including:

identifying a first level of subspecies of the microorganism sample based on the first sequenced region; and

identifying a second level of subspecies of the microorganism sample based on the second sequenced region.

32. (Amended) A system for performing real-time infection control over a computer network, comprising:

a computer network;

a centralized database;

a remote facility connected to the computer network, the remote facility obtaining a sample of a microorganism;

a server connected to the computer network, the server

receiving sequence data for a first sequenced region of a nucleic acid from the microorganism sample,

accessing the centralized database and comparing the first sequenced region with historical sequence data stored in the centralized database,

determining a measure of phylogenetic relatedness between the microorganism sample and historical samples stored in the centralized database, and

transmitting infection control information based on the phylogenetic relatedness determination to the remote facility over the computer network, thereby allowing the remote facility to use the infection control information to control or prevent the spread of an infection.

33. (Amended) Computer executable software code stored on a computer readable medium, performing a method of real-time infection control over a computer network, comprising:

obtaining a sample of a microorganism;

sequencing a first region of a nucleic acid from the microorganism sample;

comparing the first sequenced region with historical sequence data stored in a centralized database;

determining a measure of phylogenetic relatedness between the microorganism sample and historical samples stored in the centralized database; and

providing infection control information based on the phylogenetic relatedness determination, thereby allowing use of the infection control information to control or prevent the spread of an infection.

Please enter the following new claims:

34. The method of claim 1, wherein the sample is obtained at a facility remote from where the sequencing is carried out.

35. The method of claim 34, wherein the remote facility is a health care facility, and a sample of a microorganism is obtained from a prospective patient before the patient is admitted to the health care facility and exposed to patients in the health care facility.

36. The method of claim 1, wherein the sample is obtained at a facility remote from